APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/292,437	04/15/99	SCHNEEWIND	O 510015.213

HM22/1004

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	EXAMINER
	NAVARRO, A

ART UNIT	PAPER NUMBER
1645	12

DATE MAILED:
10/04/00

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

DEA/FCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER
	12

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The reply filed July 24, 2000 is not fully responsive to the

communication mailed June 19, 2000 for the reason(s) set forth on the attached

Notice To Comply With The Sequence Rules or CRF Diskette Problem Report.

Since the above-mentioned reply appears to be *bona fide*, applicant is

given a TIME PERIOD of **ONE (1) MONTH** or **THIRTY (30) DAYS**, from the mailing

date of this notice, whichever is longer, within which to supply the omission

or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME LIMIT

MAY BE GRANTED UNDER 37 CFR 1.136(a).

Mark Navarro

Primary Examiner

September 12, 2000

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An _initial_ or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An _initial_ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/292,437_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                                 This may occur if your file was retrieved in a word processor after creating it.
                                 Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
                                 This may occur if your file was retrieved in a word processor after creating it.
                                 Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
         Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                                 Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                                 As per the rules, each n or Xaa can only represent a single residue.
                                 Please present the maximum number of each residue having variable length and
                                 indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                                 sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                                 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                                 to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
                                 sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
         (OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
                                 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                                 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                                 This sequence is intentionally skipped

                                 Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
         (NEW RULES)   **<210> sequence id number**
                                 <400> sequence id number
                                 000

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
          (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                                 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
          (NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
          (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                                 Please explain source of genetic material in <220> to <223> section.
                                 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
                                 file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                                 Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

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           RAW SEQUENCE LISTING              DATE: 07/31/2000
           PATENT APPLICATION:  US/09/292,437    TIME: 15:11:23

           Input Set : A:\510015-213 Rev Seq Listing.txt
           Output Set: N:\CRF3\07312000\I292437.raw

        4 <110> APPLICANT: Olaf Schneewind
        5        Sarkis Mazmanian
        6        Gwen Liu
        7        Hung Ton-That
        9 <120> TITLE OF INVENTION: TITLE OF INVENTION: IDENTIFICATION OF SORTASE GENE
       12 <130> FILE REFERENCE: FILE REFERENCE: 510015-213
W--> 13 <140> CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/292,437
C--> 14 <141> CURRENT FILING DATE: 1999-04-15
E--> 15 <160> NUMBER OF SEQ ID: NUMBER OF SEQ ID NOS: 36
E--> 15 <160> NUMBER OF SEQ ID NOS: NUMBER OF SEQ ID NOS: 36
       17 <170> SOFTWARE: SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

E--> 19 <210> SEQ ID NO: SEQ ID NO 1
       20 <211> LENGTH: LENGTH: 5
E--> 21 <212> TYPE: PRT
       22 <213> ORGANISM: ORGANISM: Bacteria
E--> 24 <400> SEQUENCE: SEQUENCE: 1
       25 Leu Pro Xaa Thr Gly
       26  1       5
```

misaligned amino acid numbers.

see item 10 on Err Summary Sheet

all numeric identifiers from <1207 through Sequence 36 have alphabetical headings, too. Please show ONLY the numeric identifiers. The new Sequence Rules require only the numeric identifiers. The CRF program inserts the alphabetical headings as it is processing the file.

VERIFICATION SUMMARY   DATE: 07/31/2000
PATENT APPLICATION: US/09/292,437   TIME: 15:11:25

Input Set : A:\510015-213 Rev Seq Listing.txt
Output Set: N:\CRF3\07312000\I292437.raw

L:13 M:283 W: Missing Blank Line separator, <140> field identifier
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:15 M:212 E: (34) Invalid or duplicate Sequence ID Number, Number Of Sequences Unknown
L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:21 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:24 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:34 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:445 M:283 W: Missing Blank Line separator, <400> field identifier
L:15 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (36)